

Table 4. Class prediction using Prediction Analysis of Microarrays: Consistency between hierarchical clustering and prediction for the three data sets.

No. of tumor classes [*]	Training set [†]	Test set	No. of genes [‡]	Accuracy [§]
5	Norway/Stanford	van't Veer	97	0.79
		West	58	0.88
4	Norway/Stanford	van't Veer	101	0.89
		West	54	0.88

^{*}A five-class predictor (luminal A, luminal B, basal, ERBB2, normal-like) or a four-class predictor (luminal, basal, ERBB2, normal-like) was trained on the Norway/Stanford data.

[†]The Norway/Stanford data set of 115 malignant tumors (122 experiments) were used to train the classifier.

[‡]Different subsets of genes were optimal for the two different predictors in the two different data sets.

[§]Correlation between hierarchical clustering and statistical prediction.